



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 95795

To: Susan Ungar
Location: CM1-8B05
Art Unit: 1642
Wednesday, June 04, 2003

Case Serial Number: 09/125005

From: Beverly Shears
Location: Biotech-Chem Library
CM1-1E05
Phone: 308-4994

beverly.shears@uspto.gov

Search Notes

Seq. ID 6 (09/125005) v. P04637 (SwissProt_40)

Shears, Beverly

95795

From: Hart, Edward
Sent: Wednesday, June 04, 2003 11:40 AM
T : Shears, Beverly
Subject: FW: 09/125,005

Here is a rush search that I received.

Edward

-----Original Message-----

From: Chan, Christina
Sent: Tuesday, June 03, 2003 8:46 AM
T : Ungar, Susan
Cc: Hart, Edward
Subject: RE: 09/125,005

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
308-3973
CM-1, 9B19

-----Original Message-----

From: Ungar, Susan
Sent: Tuesday, June 03, 2003 8:30 AM
To: Chan, Christina
Cc: Hart, Edward
Subject: 09/125,005

Hi

I'm working on this case now, its due this biweek.

I need a very very rush comparison of SEQ ID NO:6, human p73, with PO4637, human p53 which is a hit that was picked up in the sequence search of November 7, 2002 on SwissProt_40. It was number 24 on the list but was not printed out because I did not request a printout beyond the normally sent number.

I need this one very fast, if its quicker to do the regular search and leave out the interference search that's fine, but I would need to have hits 1-45 printed out.

Ed Hart has agreed to submit this polypeptide search for me, please send authorization directly to him.

Thanks
Susan Ungar
1642
703-305-2181
CM1-8B05

SEARCH REQUEST FORM

Requestor's

Name:

Serial

Number:

Date:

Phone:

Art Unit:

Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

STAFF USE ONLY

Date completed: 06-04-03

Searcher: Beverly C 4998

Terminal time: 30

Elapsed time:

CPU-time:

Total time: 42

Number of Searches:

Number of Databases: 2

Search Site

STIC

CM-1

Pre-S

Type of Search

N.A. Sequence

A.A. Sequence

Structure

Bibliographic

Vendors

IG Suite

STN

Dialog

APS

Geninfo

SDC

DARC/Questel

Other

GGG

Wed Jun 4 14:33:08 2003

us125006_6xp04637.rec

Ungar
09/125005 v. Page 1
P# 4637

> O < 01|0 IntelliGenetics

> O < GENALIGN - Multiple Sequence Alignment Program

Release 5.4

Wed 4 Jun 103 14:29:54 - PDT

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
SP-read factor = 50

Clustered order of selected sequences:

1. p04637 (1-393)
4. US-09-125-005-6 (1-636)

Region Alignment: (listed in Clustered order)

p04637 1 meepqsdpsvEpp15qetfsdlwklp enNv1sp1psqAMD dim1spddie
US-09-125- 1 maqstatapdqgttEh1wsslepdstyfa1PqsssrnnvgttdssMDvfhlegmttssv.
consensus maqst--P---E---S-----LPqssr-NN-----MDv-----

consensus

p04637 52 qwftdpgpdaapmpeAA ppAPAPAA PT paapapapswplssspSqtktq
US-09-125- 62 maqfnllsstmdqmsrAasasPytPehhAsvPrhspyaqsstfdtmspapv1Psntdyp
consensus -----Aasa-P--P--AAsa-Prhspy-----PS---Y-

p04637 105 GsygrflglhsgtAKSVtCvTSp1nkfcQ1AKTCp1olvwdstppstrvAMalykq
US-09-125- 123 GphmpevtFqQsStAKSArtySP1kk1yCQ1AKTCp1QikvstppPGtaRmpvkk
consensus G---P---F---S-TAKS-T-TYSPL-K---CQ-AKTCP-Q---V---PPGT---RAM---YK-

p04637. 166 sqHmfevrrCPHHE Rcsdsdg1APPQHlRVEGNIrvey1DDntrfRhsVvVYEPPE
US-09-125- 184 aehvtdvVxCPnElGrdfnqgqApaSHlRVEGN1sQVdpvngqsvvVYEPq
consensus --H-T-VV-RCP-HElGR-----AP--HlRVEGN---Y-DD--T-R-SVvVYEP-

p04637 225 VGSdCmTlHNYMCNSCmGMMNRPIL-TITLEdssGn1LGRsFevRvCACPGDRD
US-09-125- 245 VGeft1lyNfMCNSCvGMMNRPIL-TITLEEmrdGqvLGRsFEGRicACPGDRka-
consensus VG--TTI-YN-MCNSC-GGMNRPIL-TITLE--G--LGR-SFE-R-CACPGDRka-

p04637 284 teenlrkkgphelpgskRA

US-09-125- 306 edhyreqqainesskngasSKRAfkqsppavpalgagvkrhgeddty1lqrgrnfe
consensus -----KRAfkqsppavpalgagvkrhgeddty1lqrgrnfe

> O < 01|0 Intelligenetics
> O < GENALIGN - Multiple Sequence Alignment Program
Release 5.4
Wed 4 Jun 103 14:29:54 - PDT

consensus

p04637 308 1pntssPOP
US-09-125- 367 ilmkikesleme1PQP1rdsyrcqq11qrpsn1lppsygpr1spmnkvhggmnk1psv

ilmkike-----PQP1rdsyrcqq11qrpsn1lppsygpr1spmnkvhggmnk1psv

> O < 01|0 Intelligenetics
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
NUCLEIC-Res-length = 4
SP-read factor = 50

p04637 319 nqlvgqppphssaatpn19vgpgmlnhghavpangemsshsaqsmysgshctppppvh
consensus nqlvgqppphssaatpn19vgpgmlnhghavpangemsshsaqsmysgshctppppvh

p04637 319 nqlvgqppphssaatpn19vgpgmlnhghavpangemsshsaqsmysgshctppppvh
US-09-125- 428 nqlvgqppphssaatpn19vgpgmlnhghavpangemsshsaqsmysgshctppppvh
consensus nqlvgqppphssaatpn19vgpgmlnhghavpangemsshsaqsmysgshctppppvh

p04637 319 kkpPldgeETT lqirgerfemfrE1ReAL
US-09-125- 489 adps1vsfltg1gcnctsgq1qsiyhlqnltEd1GALk1peqyrtmti1wglq1LK
consensus adps1vsfltg---P---EVFTsq-----E---ALK1peqyrtmti1wglq1LK
p04637 352 dAQ AgkPGrhssh1kskkqgsSRH
US-09-125- 550 qghdystAQ1lrrsnaAtis1Gg1gelqrqrvmearhfrRHTitp1nrgqGPDeva
consensus qghdyst-AQ1lrrsnaA---GGS-----RHTit-----GPD1t-----GPD-a

p04637 394

US-09-125- 611 dfgfd1pdckarkqpikeeffteaeih
consensus dfgfd1pdckarkqpikeeffteaeih

Alignment score = -1057.00

Scoring matrix:

	1	4
1		-1066
4		